Genetic diversity of Actinobacillus lignieresii isolates from different hosts

Genetic diversity detected by analysis of amplified fragment length polymorphisms (AFLPs) of 54 Actinobacillus lignieresii isolates from different hosts and geographic localities is described. On the basis of variances in AFLP profiles, the strains were grouped in two major clusters; one comprising strains isolated from horses and infected wounds of humans bitten by horses and another consisting of strains isolated from bovine and ovine hosts. The present data indicate a comparatively higher degree of genetic diversity among strains isolated from equine hosts and confirm the existence of a separate genomospecies for A. lignieresii-like isolates from horses. Among the isolates from bovine and ovine hosts some clonal lines appear to be genetically stable over time and could be detected at very distant geographic localities. Although all ovine strains investigated grouped in a single cluster, the existence of distinct genetic lineages that have evolved specificity for ovine hosts is not obvious and needs to be confirmed in other studies.

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